

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: OHTOMO, Toshihiko SATO, Koh TSUCHIYA, Masayuki
- (ii) TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN MEDULLOBLASTOMA CELLS
- (iii) NUMBER OF SEQUENCES: 132
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Foley & Lardner
 - (B) STREET: 3000 K Street, N.W., Suite 500
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/646,265
 - (B) FILING DATE: 09-SEP-1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO PCT/JP94/01763
 - (B) FILING DATE: 19-OCT-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 5-291078
 - (B) FILING DATE: 19-NOV-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: WEGNER, Harold C.
 - (B) REGISTRATION NUMBER: 25,258
 - (C) REFERENCE/DOCKET NUMBER: 53466/184
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)672-5300
 - (B) TELEFAX: (202)672-5399
 - (C) TELEX: 904136
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG	40
(2) INFORMATION FOR SEQ ID NO:2:	
(i) SEQUENCE CHARACTERISTICS:	•
(A) LENGTH: 39 base pairs	
(B) TYPE: nucleic acid	•
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
	•
(wi) SEQUENCE DESCRIPTION, SEC ID NO.2.	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	•
ACTAGTCGAC ATGGAGWCAG ACACACTCCT GYTATGGGT	39
NOTACIONE MICONOMONO MONOMOTOCI CIIMICCOI	
(2) INFORMATION FOR SEQ ID NO:3:	
(2) 1110111111011 1011 1012 101 111111	•
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 40 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	•
(D) TOPOLOGY: linear	
	· ·
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	•
ACTAGTCGAC ATGAGTGTGC TCACTCAGGT CCTGGSGTTG	40
·	
(2) INFORMATION FOR SEQ ID NO:4:	•
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(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 43 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG

(2) INFORMATION FOR SEQ ID NO:5:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
ACTAGTCGAC ATGGATTTWC AGGTGCAGAT TWTCAGCTTC	40
(2) INFORMATION FOR SEQ ID NO:6:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
ACTAGTCGAC ATGAGGTKCY YTGYTSAGYT YCTGRGG	37
(2) INFORMATION FOR SEQ ID NO:7:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 41 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
ACTAGTCGAC ATGGGCWTCA AGATGGAGTC ACAKWYYCWG G	41
(2) INFORMATION FOR SEQ ID NO:8:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 41 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	

(A)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:		
ACTAGTCGAC ATGTGGGGAY CTKTTTYCMM TTTTTCAATT G	;	41
(2) INFORMATION FOR SEQ ID NO:9:		
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
	,	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:		
ACTAGTCGAC ATGGTRTCCW CASCTCAGTT CCTTG		35
(2) INFORMATION FOR SEQ ID NO:10:	•	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:		
ACTAGTCGAC ATGTATATAT GTTTGTTGTC TATTTCT		37
(2) INFORMATION FOR SEQ ID NO:11:		
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 38 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:		
ACTAGTCGAC ATGGAAGCCC CAGCTCAGCT TCTCTTCC		38
(2) INFORMATION FOR SEQ ID NO:12:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single		



	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
GGA'	CCCGGG TGGATGGTGG GAAGATG	27
(2)	INFORMATION FOR SEQ ID NO:13:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
ACT	AGTCGAC ATGAAATGCA GCTGGGTCAT STTCTTC	37
(2)	INFORMATION FOR SEQ ID NO:14:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
ACT	AGTCGAC ATGGGATGGA GCTRTATCAT SYTCTT	36
(2)	INFORMATION FOR SEQ ID NO:15:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	

ACTAGTCGAC ATGAAGWTGT GGTTAAACTG GGTTTTT



(2)	INFO	RMATI	ON FOR	SEQ ID 1	10:16:						
	(i)	SEOU	ENCE CH	IARACTER:	ISTICS:						
	` '				se pairs						
				nucleic	_						
	-			EDNESS:							
				GY: line							
		(2)	101010								
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	(xi)	SEQU	ENCE DE	SCRIPTIO	ON: SEQ I	D NO:16	5:	•			
	•	_			_		٠.,				
ACT	AGTCG.	AC AT	GRACTTI	G GGYTC	AGCTT GRT	TT					35
(2)	INFO	RMATT	ON FOR	SEQ ID N	IO: 17:						
(-,											
	(i)	SEQU	ENCE CH	ARACTER	STICS:						•
		(A)	LENGTH	: 40 bas	e pairs						
				nucleic							
				EDNESS:							
				GY: line							
		` '				•					
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	-				•		•	•			
			•								
	(xi)	SEQU	ENCE DE	SCRIPTIO	N: SEQ I	D NO:17	':				
ACTA	AGTCG	AC AT	GGACTCC	A GGCTCA	ATTT AGT	тттссті	•				40
(2)	INFO	RMATI	ON FOR	SEQ ID N	0:18:			•			
	(i)			ARACTERI							
				: 37 bas							
		(B)	TYPE:	nucleic	acid						
		(C)	STRAND	EDNESS:	single						
	•	(D)	TOPOLO	GY: line	ar		•				
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	(xi)	SEQU	ENCE DE	SCRIPTIC	N: SEQ I	D NO:18	3:				
АСТА	AGTCG?	ልሮ ልጥ	GGCTGTC	Y TRGSGC	TRCT CTT	CTGC	,				37
	.0100.		0001010	1 11.0000	INOI OII	0100					
(2).	INFO	RMATI	ON FOR	SEQ ID N	0:19:					•	
	1:1	CECIT	בארפ כיי	7 D 7 CM 20 T	CTTCC.						•
	(1)			ARACTERI							
				: 36 bas							
				nucleic							
_				EDNESS:							
		(D)	TOPOLO	GY: line	ar						

(b)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:		
ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT		36
(2) INFORMATION FOR SEQ ID NO:20:		
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
•	• ,	
	•	,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:		
ACTAGTCGAC ATGAGAGTGC TGATTCTTTT GTG		33
(2) INFORMATION FOR SEQ ID NO:21:		
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:		40
(2) INFORMATION FOR SEQ ID NO:22:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid		
(C) STRANDEDNESS: single (D) TOPOLOGY: linear		•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:		
ACTAGTCGAC ATGGGCAGAC TTACATTCTC ATTCCTG	·	37
(2) INFORMATION FOR SEQ ID NO:23:		
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 38 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear		



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
ACTAGTCGAC ATGGATTTTG GGCTGATTTT TTTTATTG	. 38
(2) INFORMATION FOR SEQ ID NO:24:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
ACTAGTCGAC ATGATGGTGT TAAGTCTTCT GTACCTG	37
(2) INFORMATION FOR SEQ ID NO:25:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
GGATCCCGGG CCAGTGGATA GACAGATG	_ 28
(2) INFORMATION FOR SEQ ID NO:26:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 382 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

			GTC Val						48
			GTG Val						96
			GTC Val					. 1	44
			TGG Trp 55						.92
			GCA Ala					2	40
			TCT Ser						88
			 TTG Leu					3	36
			 GGT Gly					3	81
С			•		*			3	82

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Ser His Ile Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser 1 5 10 15

Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser 20 25 30

Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn 35 40 45

. Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro 50 55 60

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Lys 65	Pro	Leu	Ile	Tyr	Ser 70	Ala	Ser	Tyr	Arg	Tyr 75	Ser	Gly	Val	Pro	Asp 80		
Arg	Phe	Thr	Gly	Ser 85	Gly	Ser	Gly	Thr	Asp 90	Phe	Thr	Leu	Thr	Ile 95	Thr		
Asn	Val	Gln	Ser 100	Glu	Asp	Leu	Ala	Asp 105	Tyr	Phe	Cys	Gln	Gln 110	Tyr	Asn		,
Ser	Tyr	Pro 115	Arg	Ala	Phe	Gly	Gly 120	Gly	Thr	Lys	Leu	Glu 125	Ile	Lys			
(2)	INFO	ORMA'	TION	FOR	SEQ	ID I	NO:28	В:									
	(i)	(1 (1	A) L1 B) T1 C) S1	CE CI ENGTI YPE: IRANI OPOLO	H: 40 núcl DEDNE	09 ba Leic ESS:	ase pacion	pairs 1	3			•					
	(ix)	(1	•	E: AME/I DCAT:			108										
	(ix)	(2				_	_	tide									
	(xi)	SEQ	QUENC	CE DI	ESCRI	PTIC	ои: 3	SEQ 1	D NO	28:	:						
								TTC Phe									4.8
								CAG Gln 25									9
								TGC									14
								AAG Lys									19:
								GCG Ala								٠	240
								ATA Ile									.288





		CTC Leu							336
 	 	 GCC Ala	 						384
 	 	 GTC Val	 	G					409

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly
1 5 10 15

Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys 20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile 35 40 45

Lys Asp Thr Tyr Ile His Trp Ala Lys Gln Arg Pro Glu Gln Gly Leu 50 60

Glu Trp Ile Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp 65 70 75 80

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn 85 90 95

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val 100 105 110

Tyr Tyr Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Ser Val Thr Val Ser Ser 130 135

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

B

	,
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
GATAAGCTTC CACCATGGGC TTCAAGATGG AGTC	34
(2) INFORMATION FOR SEQ ID NO:31:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
GGCGGATCCA CTCACGTTTG ATTTCCAGTT TGGT	34
(2) INFORMATION FOR SEQ ID NO:32:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 43 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	-
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
GATAAGCTTC CACCATGAAA TGCAGCTGGG TCATGTTCTT CCT	43
(2) INFORMATION FOR SEQ ID NO:33:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
GGCGGATCCA CTCACCTGAG GAGACGGTGA CTGA	_ 34
(2) INFORMATION FOR SEQ ID NO:34:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCCTATCGGT ACAGTGGTGT GCCAAGCAGA TTCAGCGG

(D) TOPOLOGY: linear		
(will emotioned Description, SEC ID NO.34.	•	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:		
CAGACAGTGG TTCAAAGT		18
(2) INFORMATION FOR SEQ ID NO:35:		
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
	,	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:		
GAATTCGGAT CCACTCACGT TTGATT		26
(2) INFORMATION FOR SEQ ID NO:36:		
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 44 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:		
AGTCAGAATG TGGGTACTAA TGTAGCCTGG TACCAGCAGA AGCC		44
(2) INFORMATION FOR SEQ ID NO:37:		
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
·	•	

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 47 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
GCTACCTACT ACTGCCAGCA ATATAACAGC TATCCTCGGG CGTTCGG	47
(2) INFORMATION FOR SEQ ID NO:39:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 44 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
ACATTAGTAC CCACATTCTG ACTGGCCTTA CAGGTGATGG TCAC	44
(2) INFORMATION FOR SEQ ID NO:40:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 47 base pairs	
(B) TYPE: nucleic acid	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(B) TYPE: nucleic acid	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	47
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	47
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG	47
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG (2) INFORMATION FOR SEQ ID NO:41:	47
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG (2) INFORMATION FOR SEQ ID NO:41: (i) SEQUENCE CHARACTERISTICS:	47
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG (2) INFORMATION FOR SEQ ID NO:41: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	47
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG (2) INFORMATION FOR SEQ ID NO:41: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 base pairs (B) TYPE: nucleic acid	47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGA	TAGC	TGT	TATA	TTGC	TG G	CAGT	AGTA	G GT	AGCG	ATGT	CCT	С					44
(2)	INF	ORMA	TION	FOR	SEQ	ID	NO: 4	2:			-					•	
	(i	(QUEN A) L B) T C) S D) T	ENGT YPE: TRAN	H: 3 nuc DEDN	79 b leic ESS:	ase aci dou	pair d	S			-					
•			,														
	(ix) FE	ATUR	E:								•					
		-	A) N. B) L				378			٠	•						
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	(xi) SE	QUEN	CE D	ESCR:	IPTIO	ON:	SEQ :	ID No	0:42	:						
ATG	GGA	TGG	AGC	тст	ATC	ATC	CTC	TCC	TTG	GTA	GCA	ACA	GCT	ACA	GGT		48
														Thr -5			
														AGC Ser			96
Val	urs	Ser	Asp 1	iie	GIII	Met	5	GIN	Ser	PIO	ser	10	Leu	ser	Ala		
														AAT			144
Ser	Val 15	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Lys	A1a 25	Ser	Gln	Asn	Val		
														CCA			192
30	1111		·	,	35	ıyı	. GIII	GIII	БУБ	40	GIY	БУЗ	NIG	Pro	45		
														AGC			240
Leu	Leu	Ile	Tyr	Ser 50	Ala	Ser	Tyr	Arg	Tyr 55	Ser	Gly	Val	Pro	Ser 60	Arg		
														AGC			288
Phe	Ser	GLY	Ser 65	Gly	Ser	Gly	Thr	. 70	Phe	Thr	Pne	Thr	75	Ser	Ser		
														AAC			336
Leu	Gln	Pro 80	Glu	Asp	Ile	Ala	Thr 85	Tyr	Tyr	Cys	Gln	Gln 90	Tyr	Asn	Ser		
			GCG														378
Tyr	Pro 95	Arg	Ala	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys				
С																•	379

(g)

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

31

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

- (2) INFORMATION FOR SEQ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTACCGACT ACACCTTCAC CATCAGCAGC C

- (2) INFORMATION FOR SEQ ID NO:45:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
GGTGAAGGTG TAGTCGGTAC CGCTACCGCT A	31
(2) INFORMATION FOR SEQ ID NO:46:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 379 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ix) FEATURE:	
(A) NAME/KEY: CDS	
(B) LOCATION: 1378	
(ix) FEATURE:	
(A) NAME/KEY: mat_peptide (B) LOCATION: 58378	
	·
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	96
5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	192
30 35 40 45	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 50 55 60	
TTC AGC GGT AGC GGT AGT GGT ACC GAC TAC ACC TTC ACC ATC AGC AGC Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser	288
65 70 75	

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

336

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TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

378

С

379

- (2) INFORMATION FOR SEQ ID NO:47:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

- (2) INFORMATION FOR SEQ ID NO:48:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCTACCTACT TCTGCCAGCA ATATAACAG

29

(2) INFORMATION FOR SEQ ID NO:49:



(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

		(c) s:	ranı	nuc: DEDNI DGY:	ESS:	sing									
	,															
	(xi) SE	QUENC	CE D	ESCR	IPTIC	ON: S	SEQ :	ID NO	D:49	:					
TGC	rggc	AGA Z	AGTAG	GTA	GC G	ATGT	CCTC	-								29
(2)	INF	ORMA!	CION	FOR	SEQ	ID I	NO:50):						-		
	(i	(1	A) L1 3) T1 2) S1	engti Pe: Prani	HARAG H: 3' nucl DEDNI DGY:	79 ba leic ESS:	ase p acid doub	pairs 1	5							
	(ix	•	A) N2	AME/I	KEY: ION:		378			* *					·	
	(ix)		A) N2	AME/I	KEY:	_		ide				•				
	(xi) SEÇ	ONENC	CE DI	ESCR	PTIC	ON: S	SEQ I	ID NO	50:50	:					
		TGG Trp														48
		TCC Ser														96
		GGT Gly														144
		AAT Asn														192
		ATC Ile														240
		GGT Gly														288

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

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(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS



(B) LOCATION: 1..378

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

	G GGA E Gly 9								48	3
	C CAC L His								96	5
	C GTG Val								144	1
	T ACT Thr								192	2
	CTG Leu								240	כ
	AGC Ser								288	3
	CAG Gln								336	5
	CCT Pro 95								378	3
c									379	•

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10



	Val	His	Ser	Asp	Ile	Gln	Met	_	Gln	Ser	Pro	Ser		Leu	Ser	Ala	
	Co	17-1	C1.	7	3 w.c.	1703	Ωb	5 T10	Th⊷	Cvc	T ***	71-	10	Cln	Aar	Wa l	
	ser	15	GIA	Asp	Arg	vai	20	iie	Thr	Cys	rys	Ala 25	ser	GIN	Asn	Val	
	Gly 30	Thr	Asn	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	
		T.e.11	Tle	Tvr	Ser		Ser	ጥvr	Ara	Tvr		Gly	Val	Pro	Ser		
	Leu			, - , -	50		001	-1-	9	55		-			60		
	Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Tyr	Thr	Phe	Thr	Ile 75	Ser	Ser	
	Leu	Gln	Pro 80	Glu	Asp	Ile	Ala	Thr 85	Tyr	Phe	Cys	Gln	Gln 90	Tyr	Asn	Ser	
	Tyr	Pro 95	Arg	Ala	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys			
	(2)	INFO	RMAT	поі	FOR	SEQ	ID 1	10:54	1:								
		(i)	(E	A) LE B) TY C) SI	engti (PE: TRANI	HARACH: 29 nucl DEDNE	bas Leic ESS:	se pa acio sino	airs 1								
	`	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	ON: S	SEQ I	D NO	54:	:					
	TGAC	AGAG	TG I	CCGI	CACC	T GI	TAAGO	CCA									29
•	(2)	INFO	RMAT	CION	FOR	SEQ	ID N	10:55	5:			•					
		(i)	(E	A) LE B) TY C) SI	NGTH PE: RANI	HARAC H: 29 nucl DEDNE	bas leic ESS:	se pa ació sino	irs 1					÷			

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTACAGGTGA CGGACACTCT GTCACCCAC

- (2) INFORMATION FOR SEQ ID NO:56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..378

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

		AGC Ser								4	48
		GAC Asp						•			96
		GAC Asp								14	44
		GTA Val								19	92
_		TAC Tyr	_							24	40
		AGC Ser 65								28	38
		GAG Glu								33	36
		GCG Ala	-							37	78
С										37	79

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57: Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -10 -15 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 50 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 85 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 (2) INFORMATION FOR SEQ ID NO:58: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..378 (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

	TGG Trp	 	 						48
Val	 TCC Ser	 	 	 	 				96
	 GGT Gly	 	 	 	 	 	 		144

		AAT															192
30 GTÅ	Thr	Asn	Val	Ala	35	Tyr	GIn	Gin.	гÀг	40	GIÀ	гЛя	Ala	Pro	45		
		ATC															240
Leu	Leu	Ile	Tyr	Ser 50	Ala	Ser	Tyr	Arg	Tyr 55	Ser	Gly	Val	Pro	Ser 60	Arg		
TTC	AGC	GGT	AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC		288
Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Phe	Thr	Ile 75	Ser	Ser	`	
CTC	CAG	CCA	GÀG	GAC	ATC	GCC	ACC	TAC	TTC	TGC	CAG	CAA	TAT	AAC	AGC		336
Leu	Gln	Pro 80	Glu	Asp	Ile	Ala	Thr 85	Tyr	Phe	Cys	Gln	Gln 90	Tyr	Asn	Ser		
TAT	CCT	CGG	GCG	TTC	GGC	CAA	GGG	ACC	AĄG	GTG	GAA	ATC	AAA				378
Tyr	Pro 95	Arg	Ala	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys				
С		٠															379
		•											•				

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

		CAC TCC GAC ATC CAG ATG ACC CAG ACH His Ser Asp Ile Gln Met Thr Gln Ser 1					96
·	Met -19	Gly Trp Ser Cys Ile Ile Leu Ser Le	eu Val Ala 10	Thr Ala	Thr G	ly 	-
	ATG	(xi) SEQUENCE DESCRIPTION: SEQ ID		ACA GCT	ACA G	GT	48
		<pre>(ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 58378</pre>		•			
		(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1378					
			٠.				
		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 379 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear					
	(2)	INFORMATION FOR SEQ ID NO:62:					
-	CTG	CTGATGG TCAAGGTGAA GTCGGT		•			26
		(xi) SEQUENCE DESCRIPTION: SEQ ID	NO • 61 •				
		(0, 00000000000000000000000000000000000					
		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 26 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear					
	(2)	INFORMATION FOR SEQ ID NO:61:					
	GAC	TTCACCT TGACCATCAG CAGCCT					26
		(xi) SEQUENCE DESCRIPTION: SEQ ID	NO:60:				
•							
		(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 26 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear					
	(2)	INFORMATION FOR SEQ ID NO:60:					

(A)

							AAT Asn	144
							CCA Pro	192
							AGC Ser 60	240
							AGC Ser	288
		•					AAC Asn	336
						ATC Ile		378
С								3.79

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 . 5 10

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

							GCA Ala			48
							AGC Ser		_	96
		 	 	 Ile	-		GCC Ala 25			144
	•						GGA Gly			192
							GGT Gly			240
		 	 	 			TTG Leu			288
							CAG Gln			336
		 	 	 		 	GAA Glu 105			378



- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

29

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

- (2) INFORMATION FOR SEQ ID NO:66:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGACAGAGTC CAAAGCCGCT GATCTACTC

- (2) INFORMATION FOR SEQ ID NO:67:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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	(xi	.) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	10:67	: •						
ATC	AGCG	GCT	TTGG	ACTO	TG I	CCTG	GCTI	:		(29
(2)	INF	ORMA	TION	FOR	SEQ	ID	NO: 6	8:	."								
	(i	(QUEN A) L B) T C) S D) T	ENGT YPE: TRAN	H: 3 nuc DEDN	79 b leic ESS:	ase aci dou	pair d	S .								
	(ix) FE	ATUR	E:										•			
			A) N B) L														
					10		370										
	(ix	•	ATUR A) N		KEY:	mat	pep	tide									-
			B) L							·							•
																-	
	(xi) SE	QUEN	CE D	ESCR	IPTI(ON:	SEQ	ID N	0:68	:						
			AGC Ser														48
-19		11.5	501	-15	116	116	Dea	361	-10	Val	AIG	1112	nia	-5	GIÀ		
			GAC														96
Val	His	Ser	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala		
AGC	GTG	GGT	GAC	AGA	GTG	TCC	GTC	ACC	TGT	AAG	GCC	AGT	CAG	AAT	GTG		144
Ser	Val 15	Gly	Asp	Arg	Val	Ser 20	Val	Thr	Cys	Lys	Ala 25	Ser	Gln	Asn	Val		
GGT	ACT	ААТ	GTA	GCC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	ል ርጥ	CCA	AAG		192
Gly			Val		Trp					Pro							102
.30					35					40				•	45		
			TAC Tyr														240
- 			-1-	50		JUL	-1-	114.9	55	OGI	GLY	AGT	110	. 60	vrd		
			AGC														288
Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75	Ser	Ser		

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser 80 85 90

- 74 -TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 С (2) INFORMATION FOR SEQ ID NO:69: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 126 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -15 -10

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 20

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 35

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 55

Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

- (2) INFORMATION FOR SEQ ID NO:70:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GAGGACATCG CTGACTACTT CTGCCA

378

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDENNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71: AAGTAGTCAG CGATGTCCTC TGGCTG (2) INFORMATION FOR SEQ ID NO:72: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TYPE: nucleic acid (C) STRANDENNESS: double (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1378 (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 58378 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72: ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -19 -15 GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTC AGC GCC Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGA CAG AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 20 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCG GAG AGG CCA AAG GGT CAA AAG GGT ATCA AGT GTG TACT AAT GTA GCC TGG TAC CAG CAG AAG CAG AGT CCA AAG GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCC GGA CAG AGT CCA AAG GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCC GGA CAG AGT CCA AAG GTG TACT AAT GTA GCC TGG TAC CAG CAG AAG CCC GGA CAG AGT CCA AAG GTG TACT AAT GTA GCC TGG TAC CAG CAG AAG CCC GGA CAG AGT CCA AAG GTG TACT AAT GTA GCC TGG TAC CAG CAG AAG CCC GGA CAG AGT CCA AAG GTG TACT AAT GTA GCC TGG TAC CAG CAG AAG CCC GGA CAG AGT CCA AAG GTG TACT AAT GTA GCC TGG TAC CAG CAG AAG CCC GGA CAG AGT CCA AAG GTG TACT AAT GTA GCC TGG TAC CAG CAG AAG CCC GGA CAG CAG AAG CCC TGG TACT AAT GTA GCC TGG TACT CAG TAC CAG TACT GGT TACT GGT TACT CGG TAC CAG TACT GGT TACT CAG TACT GGT TACT CGG TAC CAG TACT GGT TACT CAG TACT GAG AGA CACC CTG TACT CGG TACT TACT		(2)	INF	ORMA	ATION	FOF	SEÇ	ID	NO:7	71:				•					
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ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10 -5 GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10 AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg																			
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10 -5 GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10 AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg		*																	
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10 -10 -5 GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10 AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg			(xi) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ :	ID N	0:72	:						
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg																			48
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10 AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg			Gly	Trp	Ser		Ile	Ile	Leu	Ser		Val	Ala	Thr	Ala		Gly		
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10 AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg		GTC	CAC	TCC	CAC	አመሮ	CAC	እ ጥ ር	N.C.C	CAC	200	CCA	200	700	CMC	200	cca		0.6
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg																			90
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg					1				5					10					
25 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	-																	1	144
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg		Ser		Gly	Asp	Arg	Val		Val	Thr	Cys	Lys		Ser	Gln	Asn	Val		
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg																		,	
30 35 40 45 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240 Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg		_																	192
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg								-1-			_15		1	~=			_		
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg		CCG	CTG	ATC	TAC	TCG	GCA	TCC	TAT	CGG	TAC	AGT	GGT	GTG	CCA	AGC	AGA		240
						Ser					Tyr					Ser			

TTC AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC

Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser

70

65

288

CTC CAG CCA GAG GAC ATC GCC GAC TAC TTC TGC CAG CAA TAT AAC AGC
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

C 336

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 40 45

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS



(B) LOCATION: 1..378

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

													•				
												ACA Thr					48
GTC				ATC		-	-		AGC			AGC		AGC			96
Val	His	Ser	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala		
												AGT Ser					144
	ACT					TAC					GGA	AAG					192
30	Thr	Asn	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	-	
												GTG Val					240
				GGT					TTC			ACC Thr		AGC			288
			65				-	70					75				
												CAA Gln 90					336
												ATC Ile					378
c	95			-	•	100	- 4			-	105						379
C							*										3/9

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

His	Ser	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	
Val 15	Gly	Asp	Arg	Val	Ser 20	Val	Thr	Cys	Lys	Ala 25	Ser	Gln	Asn	Val	
	Asn	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	
Leu	Ile	Tyr	Ser 50	Ala	Ser	Tyr	Arg	Tyr 55	Ser	Gly	Val	Pro		_	
Ser	Gly	Ser 65	Gly	Ser	Gly	Thr			Thr	Leu	Thr	Ile 75	Ser	Ser	
Gln	Pro 80	Glu	Asp	Ile	Ala	Asp 85	Tyr	Phe	Суз	Gln	Gln 90	Tyr	Asn	Ser	· .
Pro 95	Arg	Ala	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys			
INF	ORMAT	rion	FOR	SEQ	ID I	10:7	5:							•	
(i) SEC	OUEN	E CE	HARAG	CTER	ISTIC	cs:								
\ - .	(2	A) LI	ENGTI	H: 31	79 ba	ase p	pair	3							
	•										•				
		-													
		•													
,															
(ix)	(<i>F</i>	A) NZ	AME/I			378									
(ix)	FE#	ATURE	Ξ:												
	(P	A) NA	AME/I				ide	·						•	
(xi)	SEC	QUENC	CE DE	ESCRI	PTIC	on: s	SEQ 1	ID NO	76:	:					
															48
Gly	Trp	Ser	Cys -15	Ile	Ile	Leu	Ser	Leu -10	Val	Ala	Thr	Ala		-	
															96
His	Ser	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	
															144
እርጥ	ידעע	CTD	000	maa											
AC I	WI	GIA	GCC	TGG	TAC	CAG	CAG.	AAG	.CCA	GGA.	CAG	_AGT_	CCA	AAG	192
	Val 15 Thr Leu Ser Gln Pro 95 INF((ix) (ix) (ix) CAC His GTG Val	Val Gly 15 Thr Asn Leu Ile Ser Gly Gln Pro 80 Pro Arg 95 INFORMA: (i) SEG (i) (ix) FEA (ix) FEA (ix) SEG GGA TGG GGly Trp CAC TCC His Ser GTG GGT Val Gly	Val Gly Asp 15 Thr Asn Val Leu Ile Tyr Ser Gly Ser 65 Gln Pro Glu 80 Pro Arg Ala 95 INFORMATION (i) SEQUENC (A) Li (B) TO (C) SO (D) TO (ix) FEATURE (A) NE (B) LO (xi) SEQUENC (A) Li (B) TO (C) SO (D) TO CAC TCC GAC His Ser Asp 1 GTG GGT GAC Val Gly Asp	Val Gly Asp Arg 15 Thr Asn Val Ala Leu Ile Tyr Ser 50 Ser Gly Ser Gly 65 Gln Pro Glu Asp 80 Pro Arg Ala Phe 95 INFORMATION FOR (i) SEQUENCE CR (A) LENGTR (B) TYPE: (C) STRANK (D) TOPOLO (ix) FEATURE: (A) NAME/R (B) LOCATR (ix) FEATURE: (A) NAME/R (B) LOCATR (xi) SEQUENCE DR (xi) SEQUENCE DR GGA TGG AGC TGT Gly Trp Ser Cys —15 CAC TCC GAC ATC His Ser Asp Ile 1 GTG GGT GAC AGA Val Gly Asp Arg	Val Gly Asp Arg Val 15 Thr Asn Val Ala Trp 35 Leu Ile Tyr Ser Ala 50 Ser Gly Ser Gly Ser 65 Gln Pro Glu Asp Ile 80 Pro Arg Ala Phe Gly 95 INFORMATION FOR SEQ (i) SEQUENCE CHARAC (A) LENGTH: 3 (B) TYPE: nuc (C) STRANDEDNI (D) TOPOLOGY: (ix) FEATURE: (A) NAME/KEY: (B) LOCATION: (ix) FEATURE: (A) NAME/KEY: (B) LOCATION: (xi) SEQUENCE DESCRI	Val Gly Asp Arg Val Ser 15 20 Thr Asn Val Ala Trp Tyr 35 Leu Ile Tyr Ser Ala Ser 50 Ser Gly Ser Gly Ser Gly 65 Gln Pro Glu Asp Ile Ala 80 Pro Arg Ala Phe Gly Gln 95 100 INFORMATION FOR SEQ ID I (i) SEQUENCE CHARACTER (A) LENGTH: 379 ba (B) TyPE: nucleic (C) STRANDEDNESS: (D) TOPOLOGY: line (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1 (ix) FEATURE: (A) NAME/KEY: mat (B) LOCATION: 58 (xi) SEQUENCE DESCRIPTION GGA TGG AGC TGT ATC ATC Gly Trp Ser Cys Ile Ile —15 CAC TCC GAC ATC CAG ATG His Ser Asp Ile Gln Met 1 GTG GGT GAC AGA GTG TCC Val Gly Asp Arg Val Ser	Val Gly Asp Arg Val Ser Val 15 20 Thr Asn Val Ala Trp Tyr Gln 35 Leu Ile Tyr Ser Ala Ser Tyr 50 Ser Gly Ser Gly Ser Gly Thr 65 Gln Pro Glu Asp Ile Ala Asp 80 85 Pro Arg Ala Phe Gly Gln Gly 95 100 INFORMATION FOR SEQ ID NO:70 (i) SEQUENCE CHARACTERISTIC (A) LENGTH: 379 base 1 (B) TYPE: nucleic acid (C) STRANDEDNESS: doub (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1378 (ix) FEATURE: (A) NAME/KEY: mat_pept (B) LOCATION: 58378 (xi) SEQUENCE DESCRIPTION: SEQUENCE CONTINE SEQUENC	Val Gly Asp Arg Val Ser Val Thr 15	Val Gly Asp Arg Val Ser Val Thr Cys 15 20 Thr Asn Val Ala Trp Tyr Gln Gln Lys 35 Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr 50 55 Ser Gly Ser Gly Ser Gly Thr Asp Phe 65 70 Gln Pro Glu Asp Ile Ala Asp Tyr Phe 80 85 Pro Arg Ala Phe Gly Gln Gly Thr Lys 95 100 INFORMATION FOR SEQ ID NO:76: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TypE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1378 (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 58378 (xi) SEQUENCE DESCRIPTION: SEQ ID NO GGA TGG AGC TGT ATC ATC CTC TCC Gly Trp Ser Cys Ile Ile Leu Ser Leu -15 -10 CAC TCC GAC ATC CAG ATG ACC CAG AGC His Ser Asp Ile Gln Met Thr Gln Ser 1 5 GTG GGT GAC AGA GTG TCC GTC ACC TGT Val Gly Asp Arg Val Ser Val Thr Cys	Val Gly Asp Arg Val Ser Val Thr Cys Lys 15 Val Gly Asp Arg Val Ser Val Thr Cys Lys 15 Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro 35 Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser 50 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr 65 Ser Gly Asp Ile Ala Asp Tyr Phe Cys 80 R5 Pro Arg Ala Phe Gly Gln Gly Thr Lys Val 95 INFORMATION FOR SEQ ID NO:76: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1378 (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 58378 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76: GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA Gly Trp Ser Cys Ile Ile Leu Ser Leu Val -15 CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA His Ser Asp Ile Gln Met Thr Gln Ser Pro 1 GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG Val Gly Asp Arg Val Ser Val Thr Cys Lys	Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala 20	Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser 15 20 25 Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys 35 40 Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val 50 55 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr 65 70 Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln 80 85 90 Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile 105 INFORMATION FOR SEQ ID NO:76: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TyPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1378 (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 58378 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76: GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr -15 -10 CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC AGC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC AGT Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser	Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln 15	Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn 15 Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro 35 Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser 50 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser 65 Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn 80 Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 INFORMATION FOR SEQ ID No:76: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TypE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: cds (B) LOCATION: 58378 (xi) SEQUENCE DESCRIPTION: SEQ ID No:76: GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr -15 CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser 10 GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn	Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25 Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 35 40 45 Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 50 55 60 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser 65 70 75 Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser 80 85 90 Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105 INFORMATION FOR SEQ ID NO:76: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TyrE: nucleic acid (C) STRANDEDMESS: double (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1378 (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 58378 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76: GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -15 -10 -5 CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 1 10 GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val

CCG	CTG	ATC	TAC	TCG	GCA	TCC	TAT	CGG	TAC	AGT	GGT	GTG	CCA	AGC	AGA	•	240
Pro	Leu	Ile	Tyr	Ser 50	Ala	Ser	Tyr	Arg	Tyr 55	Ser	Gly	Val	Pro	Ser 60	Arg		
			AGC														288
Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Phe	Thr	Ile 75	Ser	Ser		
CTC	CAG	CCA	GAG	GAC	ATC	GCC	ACC	TAC	TAC	TGC	CAG	CAA	TAT	AAC	AGC	~	336
			Glu														,
TAT	CCT	CGG	GCG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA				378
			Ala														
C.																	379
(2)	TNEC	.D.V.Z.0	ITON		220												

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

1 5 10

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:	
CAG	AGAGCCAAA AGTTCCTGAG CGCCAG	26
) INFORMATION FOR SEQ ID NO:79:	
. (2)	1) INFORMATION FOR SEQ ID NO: /9:	•
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 26 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	
	(XI) SEQUENCE DESCRIPTION: SEQ ID NO. 79.	
CTC	CAGGAACT TTTGGCTCTG GGTCAT	26
(2)) INFORMATION FOR SEQ ID NO:80:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1378	
	(ix) FEATURE:	
•	(A) NAME/KEY: mat_peptide (B) LOCATION: 58378	- -
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
	G GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA G t Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr.G 9 -15 -10	
	C CAC TCC GAC ATC CAG ATG ACC CAG AGC CAA AAG TTC CTG AGC G l His Ser Asp Ile Gln Met Thr Gln Ser Gln Lys Phe Leu Ser A 1 5 10	
	C GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT G r Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn V 15 20 25	

						TAC Tyr							192
						TCC Ser							240
						GGT Gly							288
						GCC Ala							336
						CAA Gln 100							378
С	•												379
(2)	INFC	RMAT	NOI	FOR	SEQ	ID N	10:81	L:	•				
	(i) S	EQUE	ENCE	CHAF	RACTE	RIST	CICS:	1				

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Gln Lys Phe Leu Ser Ala

1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 40 45

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105



(2) INFORMATION FOR SEQ ID NO:82:

	(i)	(A) (B) (C)	JENCE C LENGT TYPE: STRAN TOPOL	H: 29 nucl	9 base leic a ESS: s	e pa: acid sing:	irs							
			4											
									-					
	(xi)	SEQU	JENCE D	ESCR	IPTION): SI	EQ I	D N	0:82	:				
GGAG	CAGAG	TC CA	AAGCTG	CT G	ATCTAC	CTC								29
(2)	INFO	RMATI	ON FOR	SEQ	ID NO	:83:	:				•			
		(A) (B) (C)	JENCE C LENGT TYPE: STRAN TOPOL	H: 29 nucl DEDNE	Dase Leic a ESS: s	e pai cid ingl	irs							
	(xi)	SEQU	ENCE D	ESCRI	PTION	: SE	EQ I	D N	D:83	:				
ATCA	AGCAG	CT TT	GGACTC	TG TO	CTGGC	TT								29
(2)	INFO	RMATI	ON FOR	SEQ	ID NO	:84:	:		•					
	(i)	(A) (B) (C)	ENCE CI LENGTI TYPE: STRANI	H: 37 nucl DEDNE	79 bas Leic a ESS: d	e pa cid oubl	irs	3				÷	· .	•
	(ix)		URE: NAME/I			8				٠				
	(ix)		URE: NAME/I LOCAT			_	.de				-			
	(xi)	SEQU	ENCE DI	ESCRI	PTION	: SE	Q I	D NO	D:84	:				
	Gly 3		GC TGT er Cys -15											4.8
			AC ATC sp Ile											96

			ACC Thr 20						144
			TAC Tyr						192
			TCC Ser		Ser				240
			GGT Gly						288
			GCC Ala				Tyr		336
			CAA Gln 100						378
С									379



(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90



Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..378

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 58..378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

	TGG Trp								48
	TCC Ser								96
	GGT Gly								144
	AAT Asn								192
	ATC Ile								240
	GGT Gly				Phe				288
	CCA Pro 80						Tyr		336
	CGG Arg							-	378

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- (2) INFORMATION FOR SEQ ID NO:87:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

23

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

- (2) INFORMATION FOR SEQ ID NO:88:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GCTCCAAAGC CGCTGATCTA CTC

- (2) INFORMATION FOR SEQ ID NO:89:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



	(xi) SE	QUENC	CE DI	ESCRI	[PTIC	ON: S	SEQ I	D NO	2:89	•						
TAG	ATCAG	GCG (GCTT	rggao	GC CI	гт											23
(2)	INFO	ORMA!	rion	FOR	SEQ	ID 1	10:90	0:			٠						•
	(i	SEC	OUENC	CE CE	HARAC	CTER	ISTIC	cs:									
	(-	(2	A) LE	ENGTI	H: 37	79 ba	ase p	pairs	3								
		į	c) s:	CRANI	nuc] DEDNI	ESS:	doul										
		·(1) T	OPOLO	OGY:	line	ear	4.									
										•							
	(ix)		ATURE													,	
,		•			KEY: [ON:		378										
	(ix)	FEA	ATURE	C:											÷		
	(200)	(2	A) NA	AME/I	KEY:	-		ide						•	-		
		. (1	, LC	JCAI	ON:	30.	. 3 / 0										
	(xi)	SEÇ	OUENC	CE DE	ESCRI	PTIC	ON: S	SEQ 1	D NO	90:	:						
	GGA																48
Met 19	Gly	Trp	Ser	Cys -15	Ile	Ile	Leu	Ser	Leu -10	Val	Ala	Thr	Ala	Thr -5	GIŸ		
GTC	CAC	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC		96
	His																
	GTG Val																144
	15			_		20			_		25						
	ACT																192
Gly 30	Thr	Asn	Val	Ala	Trp 35	Tyr	GIn	GIn	Lys	40	GIY	ràa	Ala	Pro	45		
CCG	CTG	ATC	TAC	TCG	GCA	TCC	TAT	CGG	TAC	AGT	GGT	GTG	CCA	AGC	AGA		240
	Leu			Ser					Tyr								
				50					55								000
	AGC Ser																288
		-	65	_				70					75				
	CAG																336
Leu	Gln	Pro 80	GLu	Asp	ile	Ala	Thr 85	Tyr	туr	cys	GIN	90	ıyr	ASN	ser		

378

379

60

120

									AAG Lys							
	95					100					105			•		
С													•			
(2)	INF	ORMA:	TION	FOR	SEQ	ID I	NO:9	1:								
		(i) :	(B		NGTH:	: 120 amino	6 am:	ino a id	: acid:	5			•			-
	. (ii) 1	MOLE	CULE	TYP	E: p	rote.	in					-			•
	(:	xi) s	SEQUI	ENCE	DESC	CRIP:	rion	; SEQ	Q ID	NO:	91:					•
Met -19	Gly	Trp	Ser	Cys -15		Ile	Leu	Ser	Leu -10	Val	Ala	Thr	Ala	Thr -5	Gly	
Val	His	Ser	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10		Ser	Ala	,
Ser	Val 15	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Lys	Ala 25	Ser	Gln	Asn	Val	
Gly 30	Thr	Asn	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	
Pro	Leu	Ile	Tyr	Ser 50	Ala	Ser	Tyr	Arg	Tyr 55	Ser	Gly	Val	Pro	Ser 60	Arg	
Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Phe	Thr	Ile 75	Ser	Ser	
Leu	Gln	Pro 80	Glu	Asp	Ile	Ala	Thr 85	Tyr	Tyr	Càa	Gln	Gln 90	Tyr	Asn	Ser	
Tyr	Pro 95	_			_				Lys		Glu 105	Ile	Lys	•		
(2)	INF	ORMA:	rion	FOR	SEQ	ID I	NO:9	2:								
	(i	(2	QUENC A) LI B) T	ENGT	H: 13	37 b	ase ;	pair	5							
		Ċ	C) Si	TRANI	DEDNI	ESS:	sin							•		
														•		
•		٠						• .								
•	(xi) SE	QUEN	CE D	ESCR:	IPTI	ON:	SEQ :	ID NO	0:92	:				. ,	

AAGAAGCCTG GGTCCTCAGT GAAGGTCTCC TGCAAGGCTT CTGGCTTCAA CATTAAAGAC

ACCTATATAC ACTGGGTGCG CCAGGCTCCA GGACAGGGCC TGGAGTGGAT GGGAAGGATT

W

GATCCTGAGG ATGGTAA	137
(2) INFORMATION FOR SEQ ID NO:93:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 111 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
TGAGATCTGA GGACACAGCC TTTTATTTCT GTGCAAGTGC CTACTATGTT AACCAGGACT	60
ACTGGGGCCA AGGGACCACT GTCACCGTCT CCTCAGGTGA GTGGATCCGA C	111
(2) INFORMATION FOR SEQ ID NO:94:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 130 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:	
ACCTTCACTG AGGACCCAGG CTTCTTCACC TCAGCTCCAG ACTGCACCAG CTGCACCTGG	60
GAGTGAGCAC CTGGAGCTAC AGCCAGCAAG AAGAAGACCC TCCAGGTCCA GTCCATGGTC	120
GAAGCTTATC	130
(2) INFORMATION FOR SEQ ID NO:95:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 132 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
AAAGGCTGTG TCCTCAGATC TCAGGCTGCT GAGCTCCATG TAGGCTGTGT TCGTGGATTC	60
GTCTGCAGTG ATTGTGACTC GGCCCTGGAA CTTCGGGTCA TATTTAGTAT TACCATCCGC	120



		- 89 -				
AGG	ATCAATC CT					132
(2)	INFORMATION FOR SEQ ID NO:96:					
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	5				
				•	•	
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:	96:			
GATA	AAGCTTC CACCATGGAC TGGAC					25
(2)	INFORMATION FOR SEQ ID NO:97:				•	
•	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	5			•	· · · · · · · · · · · · · · · · · · ·
				•		
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:	97:			
GTC	GGATCCA CTCACCTGAG GAGAC					25
(2)	INFORMATION FOR SEQ ID NO:98:					
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 409 base pair (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	cs	·			

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..408

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 58..408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATG GAC TGG ACC TGG AGG GTC TTC TTC TTG CTG GCT GTA GCT CCA GGT Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly -19 -15 -5

									, ,				·				
	CAC His															90	5
	GGG Gly 15															144	1
	GAC Asp															192	2
	TGG Trp															240)
	AAG Lys															288	3
	GCC Ala														TTT Phe	336	5
	TTC Phe 95															384	ŀ
	ACC Thr							G								409)
(2)	INFO	RMAT	NOI	FOR	SEQ	ID. N	10:99	9:									
	(i) s	(A) (B)	LEN TYF	IGTH:	RACTE : 136 amino GY: 1	ami aci	ino a		5							
	(i	.i) N	OLEC	ULE	TYPE	E: pr	otei	Ln									
	(x	i) S	EQUE	NCE	DESC	CRIPI	: NOI	SEÇ	O ID	NO:9	99:						
Met -19	Asp	Trp	Thr	Trp -15	Arg	Val	Phe	Phe	Leu -10	Leu	Ala	Val	Ala	Pro -5	Gly		
Ala	His	Ser	Gln 1	Val	Gln	Leu	Val 5	Gln	Ser	Gly	Ala	Glu 10	Val	Lys	Lys	•	
Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Phe	Ąsn	Ile		

Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp 50 55 60

. 40

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									- 91	-							. <u>.</u>
Pro	Lys	Phe	Gln 65	Gly	Arg	Val	Thr	Ile 70	Thr	Ala	Asp	Glu	Ser 75	Thr	Asn		
Thr	Ala	Tyr 80	Met	Glu	Leu	Ser	Ser 85	Leu	Arg	Ser	Glu	Asp 90	Thr	Ala	Phe		
Tyr	Phe 95	Cys	Ala	Ser	Ala	Tyr 100		Val	Asn	Gln	Asp 105	Tyr	Trp	Gly	Gln		
Gly 110	Thr	Thr	Val	Thr	Val 115	Ser	Ser						·	•			
(2)	INFO	ORMAT	CION	FOR	SEQ	ID 1	10:10	00:									
		(E (C	A) LI B) TY C) ST	ENGTH (PE: TRANI DPOLO	H: 84 nucl DEDNE DGY:	leic ESS: line	se pa acio sino ear	airs d gle									
			•							0:100							
AGC:	rtgto	CAC C	CGTC1	CCTC	CA GO	TGGT	rggro	G GTT	rcggc	STGG	TGGT	GGTI	CG G	GTGC	TGGCG		.60
GAT	CGGAC	CAT C	CAG	ATGAC	CC CF	AGG									•		84
(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	10:10	01:									
	(i)	(E	A) LE 3) TY C) S7	NGTH PE: RANE	i: 84 nucl	CTERI L bas Leic ESS: line	se pa acio sino	airs i									
	(xi)	SEC	UENC	E DE	SCRI	PTIC	ON : S	SEO 1	D NO	0:101	. .					-	
AATT	•									'		CACCA	CC P	vccc.	BAACCA		60
	CCACC																84
(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	10:10	02:									
	(i)	(E) LE 3) TY 3) SI	NGTH PE: RAND	: 34 nucl	TERI bas eic ESS: line	e pa acio sino	airs 1									

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:	,
CAGCCATGGC GCAGTGTGCA GCTGGTGCAG TCTG	34
(2) INFORMATION FOR SEQ ID NO:103:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:	
CCACCGAAC CACCACCAC TGAGGAGACG GTGACAGTGG T	41
(2) INFORMATION FOR SEQ ID NO:104:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
GGGACCACTG TCACCGTCTC CTCAGGTGGT GGTGGTTCGG G	41
(2) INFORMATION FOR SEQ ID NO:105:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:	
GGGCTCTGGG TCATCTGGAT GTCCGATCCG CCACCACCCG A	41
(2) INFORMATION FOR SEQ ID NO:106:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 44 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

\cdot	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:	
TCGGACATCC AGATGACCCA GAGCCCAAGC AGCCTGAGCG CCAG	14
(2) INFORMATION FOR SEQ ID NO:107:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:	
CAAGAATTCT TATTATTTAT CGTCATCGTC TTTGTAGTCT TTGATTTCGA CCTTGGT	5 7
(2) INFORMATION FOR SEQ ID NO:108:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 822 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	ſ
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1807	
(ix) FEATURE:	
(A) NAME/KEY: mat_peptide (B) LOCATION: 1807	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:	
ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC GCT Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala 1 5 10 15	18
GCC CAA CCA GCC ATG GCG CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu 20 25 30	9 6
GTG AAG AAG CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly 35 40 45	14

			ACC Thr									192
			ATG Met 70									240
			TTC Phe									288
			TAC Tyr									336
			TGT		Ala							384
			ACT Thr			Ser						432
			GGT Gly 150									480
			AGC Ser									528
			AAT Asn									576
			CCA Pro					-				624
			AGC Ser							GAC Asp		672
			AGC Ser 230									720
			AAC Asn								. •	768
			GAC Asp					TAAT	AAGA	AT		817
TCTT	'G	•										822

(b)

- (2) INFORMATION FOR SEQ ID NO:109:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:
- Met Lys Tyr Leu Leu Pro Thr Ala Ala Gly Leu Leu Leu Ala 1 5 10 15
- Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu 20 25 30
- Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly 35 40 45
- Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly 50 55 60
- Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr
 65 70 75 80
- Lys Tyr Asp Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 85 90 95
- Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp 100 105 110
- Thr Ala Phe Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr 115 120 125
- Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser 130 135 140
- Gly Gly Gly Gly Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln 145 150 155 160
- Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr 165 170 175
- Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln 180 185 190
- Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg 195 200 205
- Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp 210 215 220
- Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr 225 230 235 240
- Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg Ala Phe Gly Gln Gly Thr 245 250 255



Lys Val Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys 260 265

- (2) INFORMATION FOR SEQ ID NO:110:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..45
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..45
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGT GGT GGT TCG GGT GGT GGT TCG GGT GGC GGA TCG
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

45

- (2) INFORMATION FOR SEQ ID NO:111:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser

1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:112:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Tyr Gln Gln Lys Pro Gly Lys Ala
20 25 30

Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro 35 40 45

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile 50 55 60

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Phe Gly Gln 65 70 75 80

Gly Thr Lys Val Glu Ile Lys 85

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Trp Val 20 25 30

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Val Thr Ile 35 40 45

Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu 50 55 60

Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys Ala Gly 65 70 75

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO:115:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp Thr Tyr Ile His

- (2) INFORMATION FOR SEQ ID NO:116:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp Pro Lys Phe Gln

Gly

- (2) INFORMATION FOR SEQ ID NO:117:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Tyr Tyr Val Asn Gln Asp Tyr



- (2) INFORMATION FOR SEQ ID NO:118:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala 1 5 10

- (2) INFORMATION FOR SEQ ID NO:119:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Ser Ala Ser Tyr Arg Tyr Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:120:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Gln Gln Tyr Asn Ser Tyr Pro Arg Ala 1 $\,$ 5

- (2) INFORMATION FOR SEQ ID'NO:121:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: S	SEQ	ΙD	NO:121:
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys 20

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr

1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:123:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys 20 25 30

- (2) INFORMATION FOR SEQ ID NO:124:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

- (2) INFORMATION FOR SEQ ID NO:125:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr .
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:126:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid.
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys 20 25 30

- (2) INFORMATION FOR SEQ ID NO:127:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 10

- (2) INFORMATION FOR SEQ ID NO:128:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

. Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys Ala Ser 20 25 30

- (2) INFORMATION FOR SEQ ID NO:129:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser 1 10

- (2) INFORMATION FOR SEQ ID NO:130:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn 20 25

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile 35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly 50 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro 65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg 85 90 95

Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn 20 25

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile 35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly 50 55

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg 85

Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 35 40 45

Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp Pro Lys Phe 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys 85 90 95

Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln Gly Thr Thr
100 105 110

Val Thr Val Ser Ser 115

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